

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/762,258

DATE: 02/13/2001
 TIME: 15:01:20

Input Set : A:\Lu5002us.txt
 Output Set: N:\CRF3\02132001\I762258.raw

ENTERED

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3 <110> APPLICANT: Gout, Ivan
4   Hara, Kenta
5   Waterfield, Michael
6   Yonezawa, Kazu
7   Ludwig Institute for Cancer Research
9 <120> TITLE OF INVENTION: Identification and Functional Characterization of a
10  Novel Ribosomal S6 Protein Kinase
12 <130> FILE REFERENCE: 40750-5002-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/762,258
C--> 15 <141> CURRENT FILING DATE: 2001-02-05
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/17595
18 <151> PRIOR FILING DATE: 1999-08-04
20 <150> PRIOR APPLICATION NUMBER: 60/095,268
21 <151> PRIOR FILING DATE: 1998-08-04
23 <160> NUMBER OF SEQ ID NOS: 8
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1816
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (77)..(1561)
35 <223> OTHER INFORMATION: p70(beta) S6 Kinase gene
37 <400> SEQUENCE: 1
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40   gagagactcg tgccga atg gca cga ggc cga cgg gcc cgc ggg gcc ggc gcc 112
41       Met Ala Arg Gly Arg Arg Ala Arg Gly Ala Gly Ala
42       1           5           10
44   gcc atg gcg gcc gtg ttt gat ttg gat ttg gag acg gag gaa ggc agc 160
45   Ala Met Ala Ala Val Phe Asp Leu Asp Leu Glu Thr Glu Glu Gly Ser
46       15           20           25
48   gag ggc gag ggc gag cca gag ctg agc ccc gcg gac gca tgt ccc ctt 208
49   Glu Gly Glu Gly Glu Pro Glu Leu Ser Pro Ala Asp Ala Cys Pro Leu
50       30           35           40
52   gcc gag ttg agg gca gct ggc cta gag cct gtg gga cac tat gaa gag 256
53   Ala Glu Leu Arg Ala Ala Gly Leu Glu Pro Val Gly His Tyr Glu Glu
54       45           50           55           60
56   gtg gag ctg act gag acc agc gtg aac gtt ggc cca gag cgc atc ggg 304
57   Val Glu Leu Thr Glu Thr Ser Val Asn Val Gly Pro Glu Arg Ile Gly
58       65           70           75
60   ccc cac tgc ttt gag ctg ctg cgt gtg ctg ggc aag ggg ggc tat ggc 352
61   Pro His Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Tyr Gly
62       80           85           90
64   aag gtg ttc cag gtg cga aag gtg caa ggc acc aac ttg ggc aaa ata 400
65   Lys Val Phe Gln Val Arg Lys Val Gln Gly Thr Asn Leu Gly Lys Ile
66       95           100          105

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68  tat gcc atg aaa gtc cta agg aag gcc aaa att gtg cgc aat gcc aag 448
69  Tyr Ala Met Lys Val Leu Arg Lys Ala Lys Ile Val Arg Asn Ala Lys
70      110                      115                      120
72  gac aca gca cac aca cgg gct gag cgg aac att cta gag tca gtg aag 496
73  Asp Thr Ala His Thr Arg Ala Glu Arg Asn Ile Leu Glu Ser Val Lys
74  125                      130                      135                      140
76  cac ccc ttt att gtg gaa ctg gcc tat gcc ttc cag act ggt ggc aaa 544
77  His Pro Phe Ile Val Glu Leu Ala Tyr Ala Phe Gln Thr Gly Gly Lys
78      145                      150                      155
80  ctc tac ctc atc ctt gag tgc ctc agt ggt ggc gag ctc ttc acg cat 592
81  Leu Tyr Leu Ile Leu Glu Cys Leu Ser Gly Gly Glu Leu Phe Thr His
82      160                      165                      170
84  ctg gag cga gag ggc atc ttc ctg gaa gat acg gcc tgc ttc tac ctg 640
85  Leu Glu Arg Glu Gly Ile Phe Leu Glu Asp Thr Ala Cys Phe Tyr Leu
86      175                      180                      185
88  gct gag atc acg ctg gcc ctg ggc cat ctc cac tcc cag ggc atc atc 688
89  Ala Glu Ile Thr Leu Ala Leu Gly His Leu His Ser Gln Gly Ile Ile
90      190                      195                      200
92  tac cgg gac ctc aag ccc gag aac atc atg ctc agc agc cag ggc cac 736
93  Tyr Arg Asp Leu Lys Pro Glu Asn Ile Met Leu Ser Ser Gln Gly His
94  205                      210                      215                      220
96  atc aaa ctg acc gac ttt gga ctc tgc aag gag tct atc cat gag ggc 784
97  Ile Lys Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Glu Gly
98      225                      230                      235
100  gcc gtc act cac acc ttc tgc ggc acc att gag tac atg gcc cct gag 832
101  Ala Val Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu
102      240                      245                      250
104  att ctg gtg cgc agt ggc cac aac cgg gct gtg gac tgg tgg agc ctg 880
105  Ile Leu Val Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu
106      255                      260                      265
108  ggg gcc ctg atg tac gac atg ctc act gga tgc ccg ccc ttt acc gca 928
109  Gly Ala Leu Met Tyr Asp Met Leu Thr Gly Ser Pro Pro Phe Thr Ala
110      270                      275                      280
112  gag aac cgg aag aaa acc atg gat aag atc atc agg ggc aag ctg gca 976
113  Glu Asn Arg Lys Lys Thr Met Asp Lys Ile Ile Arg Gly Lys Leu Ala
114  285                      290                      295                      300
116  ctg ccc ccc tac ctc acc cca gat gcc cgg gac ctt gtc aaa aag ttt 1024
117  Leu Pro Pro Tyr Leu Thr Pro Asp Ala Arg Asp Leu Val Lys Lys Phe
118      305                      310                      315
120  ctg aaa cgg aat ccc agc cag cgg att ggg ggt ggc cca ggg gat gct 1072
121  Leu Lys Arg Asn Pro Ser Gln Arg Ile Gly Gly Gly Pro Gly Asp Ala
122      320                      325                      330
124  gct gat gtg cag aga cat ccc ttt ttc cgg cac atg aat tgg gac gac 1120
125  Ala Asp Val Gln Arg His Pro Phe Phe Arg His Met Asn Trp Asp Asp
126      335                      340                      345
128  ctt ctg gcc tgg cgt gtg gac ccc cct ttc agg ccc tgt ctg cag tca 1168
129  Leu Leu Ala Trp Arg Val Asp Pro Pro Phe Arg Pro Cys Leu Gln Ser
130      350                      355                      360
132  gag gag gac gtg agc cag ttt gat acc cgc ttc aca cgg cag acg ccg 1216

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133  Glu Glu Asp Val Ser Gln Phe Asp Thr Arg Phe Thr Arg Gln Thr Pro
134  365                               370                               375                               380
136  gtg gac agt cct gat gac aca gcc ctc agc gag agt gcc aac cag gcc 1264
137  Val Asp Ser Pro Asp Asp Thr Ala Leu Ser Glu Ser Ala Asn Gln Ala
138                               385                               390                               395
140  ttc ctg ggc ttc aca tac gtg gcg ccg tct gtc ctg gac agc atc aag 1312
141  Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val Leu Asp Ser Ile Lys
142                               400                               405                               410
144  gag ggc ttc tcc ttc cag ccc aag ctg cgc tca ccc agg cgc ctc aac 1360
145  Glu Gly Phe Ser Phe Gln Pro Lys Leu Arg Ser Pro Arg Arg Leu Asn
146                               415                               420                               425
148  agt agc ccc cgg gtc ccc gtc agc ccc ctc aag ttc tcc cct ttt gag 1408
149  Ser Ser Pro Arg Val Pro Val Ser Pro Leu Lys Phe Ser Pro Phe Glu
150                               430                               435                               440
152  ggg ttt cgg ccc agc ccc agc ctg ccg gag ccc acg gag cta cct cta 1456
153  Gly Phe Arg Pro Ser Pro Ser Leu Pro Glu Pro Thr Glu Leu Pro Leu
154  445                               450                               455                               460
156  cct cca ctc ctg cca ccg ccg ccg ccc tcg acc acc gcc cct ctc ccc 1504
157  Pro Pro Leu Leu Pro Pro Pro Pro Pro Ser Thr Thr Ala Pro Leu Pro
158                               465                               470                               475
160  atc cgt ccc ccc tca ggg acc aag aag tcc aag agg ggc cgt ggg cgt 1552
161  Ile Arg Pro Pro Ser Gly Thr Lys Lys Ser Lys Arg Gly Arg Gly Arg
162                               480                               485                               490
164  cca ggg cgc taggaagccg ggtgggggtg agggtagccc ttgagccctg 1601
165  Pro Gly Arg
166  495
168  tcacctgcggc tgtgagagca gcaggacctt gggccagttc cagagacctg ggggtgtgtc 1661
170  tgggggtggg gtgtgagtgc gtatgaaagt gtgtgtctgc tggggcagct gtgcccctga 1721
172  atcatgggca cggagggccg cccgccacac cccgcgtca actgctccg tggaagatta 1781
174  aagggtgaa tcatgaaaa aaaaaaaaaa aaaaa 1816
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178 <211> LENGTH: 495
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapiens
182 <220> FEATURE:
183 <223> OTHER INFORMATION: p70(beta) S6 Kinase protein
185 <400> SEQUENCE: 2
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189  Val Phe Asp Leu Asp Leu Glu Thr Glu Glu Gly Ser Glu Gly Glu Gly
190  20 25 30
192  Glu Pro Glu Leu Ser Pro Ala Asp Ala Cys Pro Leu Ala Glu Leu Arg
193  35 40 45
195  Ala Ala Gly Leu Glu Pro Val Gly His Tyr Glu Glu Val Glu Leu Thr
196  50 55 60
198  Glu Thr Ser Val Asn Val Gly Pro Glu Arg Ile Gly Pro His Cys Phe
199  65 70 75 80
201  Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val Phe Gln
202  85 90 95

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204 Val Arg Lys Val Gln Gly Thr Asn Leu Gly Lys Ile Tyr Ala Met Lys
205      100      105      110
207 Val Leu Arg Lys Ala Lys Ile Val Arg Asn Ala Lys Asp Thr Ala His
208      115      120      125
210 Thr Arg Ala Glu Arg Asn Ile Leu Glu Ser Val Lys His Pro Phe Ile
211      130      135      140
213 Val Glu Leu Ala Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr Leu Ile
214      145      150      155      160
216 Leu Glu Cys Leu Ser Gly Gly Glu Leu Phe Thr His Leu Glu Arg Glu
217      165      170      175
219 Gly Ile Phe Leu Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu Ile Thr
220      180      185      190
222 Leu Ala Leu Gly His Leu His Ser Gln Gly Ile Ile Tyr Arg Asp Leu
223      195      200      205
225 Lys Pro Glu Asn Ile Met Leu Ser Ser Gln Gly His Ile Lys Leu Thr
226      210      215      220
228 Asp Phe Gly Leu Cys Lys Glu Ser Ile His Glu Gly Ala Val Thr His
229      225      230      235      240
231 Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu Val Arg
232      245      250      255
234 Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala Leu Met
235      260      265      270
237 Tyr Asp Met Leu Thr Gly Ser Pro Phe Thr Ala Glu Asn Arg Lys
238      275      280      285
240 Lys Thr Met Asp Lys Ile Ile Arg Gly Lys Leu Ala Leu Pro Pro Tyr
241      290      295      300
243 Leu Thr Pro Asp Ala Arg Asp Leu Val Lys Lys Phe Leu Lys Arg Asn
244      305      310      315      320
246 Pro Ser Gln Arg Ile Gly Gly Gly Pro Gly Asp Ala Ala Asp Val Gln
247      325      330      335
249 Arg His Pro Phe Phe Arg His Met Asn Trp Asp Asp Leu Leu Ala Trp
250      340      345      350
252 Arg Val Asp Pro Pro Phe Arg Pro Cys Leu Gln Ser Glu Glu Asp Val
253      355      360      365
255 Ser Gln Phe Asp Thr Arg Phe Thr Arg Gln Thr Pro Val Asp Ser Pro
256      370      375      380
258 Asp Asp Thr Ala Leu Ser Glu Ser Ala Asn Gln Ala Phe Leu Gly Phe
259      385      390      395      400
261 Thr Tyr Val Ala Pro Ser Val Leu Asp Ser Ile Lys Glu Gly Phe Ser
262      405      410      415
264 Phe Gln Pro Lys Leu Arg Ser Pro Arg Arg Leu Asn Ser Ser Pro Arg
265      420      425      430
267 Val Pro Val Ser Pro Leu Lys Phe Ser Pro Phe Glu Gly Phe Arg Pro
268      435      440      445
270 Ser Pro Ser Leu Pro Glu Pro Thr Glu Leu Pro Leu Pro Pro Leu Leu
271      450      455      460
273 Pro Pro Pro Pro Pro Ser Thr Thr Ala Pro Leu Pro Ile Arg Pro Pro
274      465      470      475      480
276 Ser Gly Thr Lys Lys Ser Lys Arg Gly Arg Gly Arg Pro Gly Arg

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277          485          490          495
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281 <211> LENGTH: 2346
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283 <213> ORGANISM: Homo sapiens
285 <220> FEATURE:
286 <221> NAME/KEY: CDS
287 <222> LOCATION: (28)..(1602)
288 <223> OTHER INFORMATION: p70(alpha) S6 Kinase gene
290 <400> SEQUENCE: 3
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292                               Met Arg Arg Arg Arg Arg Arg Arg Asp Gly
293                               1          5
295   ttt tac cca gcc ccg gac ttc cga gac agg gaa gct gag gac atg gca 102
296   Phe Tyr Pro Ala Pro Asp Phe Arg Asp Arg Glu Ala Glu Asp Met Ala
297   10          15          20          25
299   gga gtg ttt gac ata gac ctg gac cag cca gag gac gcg ggc tct gag 150
300   Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu
301   30          35          40
303   gat gag ctg gag gag ggg ggt cag tta aat gaa agc atg gac cat ggg 198
304   Asp Glu Leu Glu Glu Gly Gly Gln Leu Asn Glu Ser Met Asp His Gly
305   45          50          55
307   gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa 246
308   Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu
309   60          65          70
311   atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa 294
312   Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu
313   75          80          85
315   tgt ttt gag cta ctt cgg gta ctt ggt aaa ggg ggc tat gga aag gtt 342
316   Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val
317   90          95          100          105
319   ttt caa gta cga aaa gta aca gga gca aat act ggg aaa ata ttt gcc 390
320   Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile Phe Ala
321   110          115          120
323   atg aag gtg ctt aaa aag gca atg ata gta aga aat gct aaa gat aca 438
324   Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys Asp Thr
325   125          130          135
327   gct cat aca aaa gca gaa cgg aat att ctg gag gaa gta aag cat ccc 486
328   Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys His Pro
329   140          145          150
331   ttc atc gtg gat tta att tat gcc ttt cag act ggt gga aaa ctc tac 534
332   Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr
333   155          160          165
335   ctc atc ctt gag tat ctc agt gga gga gaa cta ttt atg cag tta gaa 582
336   Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu
337   170          175          180          185
339   aga gag gga ata ttt atg gaa gac act gcc tgc ttt tac ttg gca gaa 630
340   Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu
341   190          195          200

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VERIFICATION SUMMARY DATE: 02/13/2001
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date